
Genome-wide prediction of transcription factor binding sites using an integrated model.

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Public Summary:

We present a computational method for the genome-wide identification of binding sites for transcription factors. This method is designed to capture the characteristic patterns of transcription factor binding motif occurrences and the chromatin signatures at regulatory elements. The method significantly outperforms other methods in the identification of 13 transcription factor binding sites in mouse embryonic stem cells.

Scientific Abstract:

We present an integrated method called Chromia for the genome-wide identification of functional target loci of transcription factors. Designed to capture the characteristic patterns of transcription factor binding motif occurrences and the histone profiles associated with regulatory elements such as promoters and enhancers, Chromia significantly outperforms other methods in the identification of 13 transcription factor binding sites in mouse embryonic stem cells, evaluated by both binding (ChIP-seq) and functional (RNA interference knockdown) experiments.

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